
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=16; hr=8; min=29; sec=11; ms=981;]

Reviewer Comments:

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

Numeric identifier <160> must reflect the total number of sequences in the sequence listing. There are only 226 sequences in this sequence listing but, <160> states there are 229. Please make all necessary changes

<210> 129

<212> PRT

<213> Artificial Sequence

<2.2.0>

<223> VEGFR-1 derived peptides

<400> 129

Lys Leu Leu Arg Gly His Thr Leu Val

Numeric identifier "<211> Length" is mandatory for each SEQ ID number.

SEQUENCE LISTING

<110>	Center for Genetic Engineering and Biotechnology	
<120>	Antiangiogenic active immunotherapies	
<130>	976-19 PCT/US/RCE	
<140>		
<141>	2004-10-15	
<150>	CU 2002/0076	
<151>	2002-04-15	
<160>	229	
<170>	PatentIn version 3.4	
<210>	1	
<211>	21	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
	primer	
	<u> </u>	
<400>	1	
tggatc	catg aactttctgc t	21
<210>	2	
	22	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	2	
gaattc	accg cctcggcttg tc	22
<210>	3	
<211>	21	
	DNA	
<213>	Artificial Sequence	
<220>		
<223>	primer	
<400>	3	
tggatc	catg aactttctgc t	21
<010:	4	
<210> <211>	4 30	

<212> DNA

```
<213> Artificial Sequence
<220>
<223> primer
<400> 4
ctggccttgt gcaggtgcga ttgccataat
                                                                   30
<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 5
attatggcaa tcgcacctgc acaaggccag
                                                                   30
<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 6
                                                                   22
gaattcaccg cctcggcttg tc
<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 7
                                                                   21
tggatccatg aactttctgc t
<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 8
                                                                   22
gaattcaccg cctcggcttg tc
```

```
<210> 9
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 9
tggatccatg gagagcaagg tgctg
                                                                   25
<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 10
                                                                   25
gaattcacat cagcccactg gatgc
<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 11
                                                                   21
cctctagatg tgcaaaagtg g
<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 12
tgagatcttc gggagcttcc
                                                                   20
<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
```

<400> 13

<210>	14
<211>	
<212>	
	Artificial Sequence
<220>	
<223>	primer
<400>	14
tagcgg	ccgc ttaaacagg
<210>	
<211>	
<212>	
\Z13>	Artificial Sequence
<220>	
	primer
-223,	F- 7
<400>	15
aggcct	ctac acctgccagg ca
<210>	16
<211>	
<212>	
<213>	Artificial Sequence
0.5.5	
<220>	
<223>	primer
<100>	1.6
<400>	
cccayy	ttaa acaggaggag
<210>	17
<211>	
<212>	
<213>	Artificial Sequence
<220>	
<223>	primer
<400>	
cccddd	atat ttataaagat c
0.1.5	
<210>	
<211>	19
<212>	DNA Artificial Sequence
ヘムエン /	Erriticial pequence

gaagatctgt ataaggactt c

<220>

<400> 18

tagcggccgc ttaaacagg 19

<210> 19

<211> 147

<212> PRT

<213> Homo Sapiens

<400> 147

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu 50 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Glu Ile Glu Pro Glu
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys 130 135 140

Pro Arg Arg

145

<210> 20

<211> 444

<212> DNA

<213> Homo Sapiens

<400> 20

atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat

120

180

gccaagtggt cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg

gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac

atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360 420 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa aaatgtgaca agccgaggcg gtga 444 <210> 21 <211> 147 <212> PRT <213> Homo Sapiens <400> 147 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu 10 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly 25 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln 35 40 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu 55 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

70 75

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Ala Ile Ala Pro Ala 100 105

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys 130 135 140

Pro Arg Arg 145

<210> 22

<211> 444

<212> DNA

<213> Homo Sapiens

<400> 22

gccaagtggt cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg	120
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac	180
atettecagg agtaccetga tgagategag tacatettea ageeateetg tgtgcccetg	240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc	300
aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg	360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa	420
aaatgtgaca agccgaggcg gtaa	444
<210> 23 <211> 314 <212> PRT <213> Homo Sapiens <400> 314	
Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu 1 5 10 15	
Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro 20 25 30	
Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr 35 40 45	
Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro 50 55 60	
Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser 65 70 75 80	
Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn 85 90 95	
Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser 100 105 110	
Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser 115 120 125	
Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys 130 135 140	
Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser 145 150 155 160	
Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg	

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile

180 185 190

 Ser
 Tyr
 Ala
 Gly
 Met
 Val
 Phe
 Cys
 Glu
 Ala
 Lys
 Ile
 Asn
 Asp
 Glu
 Ser

 Tyr
 Gln
 Ser
 Ile
 Met
 Tyr
 Ile
 Val
 Val
 Val
 Gly
 Tyr
 Arg
 Ile
 Tyr

 210
 215
 220
 220
 220
 1
 Arg
 Ile
 Tyr

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu 225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile \$245\$ \$250\$ 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu 260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe 275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu 290 295 300

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met 305

<210> 24

<211> 943

<212> DNA

<213> Homo Sapiens

<400> 24

atggagagaa aggtgctgct ggccgtcgcc ctgtggctct gcgtggagac ccgggccgcc 60 tctgtgggtt tgcctagtgt ttctcttgat ctgcccaggc tcagcataca aaaagacata 120 cttacaatta aggctaatac aactcttcaa attacttgca ggggacagag ggacttggac 180 240 tggctttggc ccaataatca gagtggcagt gagcaaaggg tggaggtgac tgagtgcagc gatggcctct tctgtaagac actcacaatt ccaaaagtga tcggaaatga cactggagcc 300 tacaagtgct tctaccggga aactgacttg gcctcggtca tttatgtcta tgttcaagat 360 tacagatete cattiatige tietgitagi gaccaacatg gagtegitgia cattactgag 420 aacaaaaaca aaactgtggt gattccatgt ctcgggtcca tttcaaatct caacgtgtca 480 ctttqtqcaa qatacccaqa aaaqaqattt qttcctqatq qtaacaqaat ttcctqqqac 540 agcaagaagg getttactat teecagetae atgateaget atgetggeat ggtettetgt 600 gaagcaaaaa ttaatgatga aagttaccag tctattatgt acatagttgt cgttgtaggg 660 720 tataggattt atgatgtggt tctgagtccg tctcatggaa ttgaactatc tgttggagaa

aago	cttgt	tct 1	caaat	tgta	ac aq	gcaaq	gaact	gaa	acta	aatg	tgg	ggatt	ga (cttca	aactgg	780
gaat	cacco	ctt (cttc	gaag	ca to	cagc	ataaq	g aa	actt	gtaa	acc	gagad	cct a	aaaa	acccag	840
tct	ggga	gtg a	agat	gaaga	aa at	tttt	cgago	c ac	ctta	acta	taga	atggt	igt a	aacc	cggagt	900
gac	caago	gat 1	gta	cacci	tg to	gcago	catco	c agi	ggg	ctga	tga					943
<210 <211 <211 <211	1> (2> I 3> I	25 611 PRT Homo	sap	iens												
			Glu	Ala	Phe	Phe	Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Thr	
1	_			5					10	_				15		
Asn	Leu	Glu	Ile 20	Ile	Ile	Leu	Val	Gly 25	Thr	Ala	Val	Ile	Ala 30	Met	Phe	
Phe	Trp	Leu 35	Leu	Leu	Val	Ile	Ile 40	Leu	Arg	Thr	Val	Lys 45	Arg	Ala	Asn	
Gly	Gly 50	Glu	Leu	Lys	Thr	Gly 55	Tyr	Leu	Ser	Ile	Val 60	Met	Asp	Pro	Asp	
Glu 65	Leu	Pro	Leu	Asp	Glu 70	His	Суз	Glu	Arg	Leu 75	Pro	Tyr	Asp	Ala	Ser 80	
Lys	Trp	Glu	Phe	Pro 85	Arg	Asp	Arg	Leu	Lys 90	Leu	Gly	Lys	Pro	Leu 95	Gly	
Arg	Gly	Ala	Phe 100	Gly	Gln	Val	Ile	Glu 105	Ala	Asp	Ala	Phe	Gly 110	Ile	Asp	
Lys	Thr	Ala 115	Thr	Суз	Arg	Thr	Val 120	Ala	Val	Lys	Met	Leu 125	Lys	Glu	Gly	
Ala	Thr 130	His	Ser	Glu	His	Arg 135	Ala	Leu	Met	Ser	Glu 140	Leu	Lys	Ile	Leu	
Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	Leu	Gly	Ala	Суз	

Thr	Lys	Pro	Gly	Gly 165	Pro	Leu	Met	Val	Ile 170	Val	Glu	Phe	Cys	Lys 175	Phe
		Leu	180		-			185	-				190		
-		Thr 195					200					205			
	210	Pro				215					220				
225		Glu			230					235	_				240
Leu	Glu	His	Leu	245 Ile	Cys	Tyr	Ser	Phe	250 Gln	Val	Ala	Lys	Gly	255 Met	Glu
Phe	Leu	Ala	260 Ser	Arg	Lys	Cys	Ile	265 His	Arg	Asp	Leu	Ala	270 Ala	Arg	Asn
Ile		275 Leu	Ser	Glu	Lys		280 Val	Val	Lys	Ile	_	285 Asp	Phe	Gly	Leu
Ala 305	290 Arg	Asp	Ile	Tyr	Lys	295 Asp	Pro	Asp	Tyr	Val 315	300 Arg	Lys	Gly	Asp	Ala 320
	Leu	Pro	Leu	Lys 325		Met	Ala	Pro	Glu 330		Ile	Phe	Asp	Arg	
Tyr	Thr	Ile	Gln 340	Ser	Asp	Val	Trp	Ser 345	Phe	Gly	Val	Leu	Leu 350	Trp	Glu
Ile	Phe	Ser 355	Leu	Gly	Ala	Ser	Pro 360	Tyr	Pro	Gly	Val	Lys 365	Ile	Asp	Glu
Glu	Phe 370	Cys	Arg	Arg	Leu	Lys 375	Glu	Gly	Thr	Arg	Met 380	Arg	Ala	Pro	Asp

Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly

385 390 395 400

Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu Gly 405 410 415

Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430$

Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser
435 440 445

Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu Val Cys Asp 450 460

Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr Leu Gln 465 470 475 480

Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp
485 490 495

Ile Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln \$500\$ \$505\$ \$510

Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu 515 520 525

Asp Arg Thr Lys Leu Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys 530 540

Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr 545 550 555 560

Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser 575

Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile Gly Val Gln Thr Gly 580 585 590

Ser Thr Ala Gln Ile Leu Gln Pro Asp Ser Gly Thr Thr Leu Ser Ser 595 600 605

Pro Pro Val

<210> 26

<211> 1836

<212> DNA

<213> Homo Sapiens

<400> 1836

gcaaaagtgg aggcattttt cataatagaa ggtgcccagg aaaagacgaa cttggaaatc 60 attattctag taggcacggc ggtgattgcc atgttcttct ggctacttct tgtcatcatc 120 ctacggaccg ttaagcgggc caatggaggg gaactgaaga caggctactt gtccatcgtc 180 atggatccag atgaactccc attggatgaa cattgtgaac gactgcctta tgatgccagc 240 300 aaatgggaat teeceagaga eeggetgaag etaggtaage etettggeeg tggtgeettt ggccaagtga ttgaagcaga tgcctttgga attgacaaga cagcaacttg caggacagta 360 420 gcagtcaaaa tgttgaaaga aggagcaaca cacagtgagc atcgagctct catgtctgaa 480 ctcaagatcc tcattcatat tggtcaccat ctcaatgtgg tcaaccttct aggtgcctgt accaagccag gagggccact catggtgatt gtggaattct gcaaatttgg aaacctgtcc 540 600 acttacctga ggagcaagag aaatgaattt gtcccctaca agaccaaagg ggcacgattc cgtcaaggga aagactacgt tggagcaatc cctgtggatc tgaaacggcg cttggacagc 660 atcaccagta gccagagctc agccagctct ggatttgtgg aggagaagtc cctcagtgat 720 gtagaagaag aggaagctcc tgaagatctg tataaggact tcctgacctt ggagcatctc 780 840 atctgttaca gcttccaagt ggctaagggc atggagttct tggcatcgcg aaagtgtatc cacagggacc tggcggcacg aaatatcctc ttatcggaga agaacgtggt taaaatctgt 900 gactttggct tggcccggga tatttataaa gatccagatt atgtcagaaa aggagatgct 960 cgcctccctt tgaaatggat ggccccagaa acaatttttg acagagtgta cacaatccag 1020 agtgacgtct ggtcttttgg tgttttgctg tgggaaatat tttccttagg tgcttctcca 1080 tatcctgggg taaagattga tgaagaattt tgtaggcgat tgaaagaagg aactagaatg 1140 agggcccctg attatactac accaga